

Claims

1. DNA sequences which contain the coding region of an amino acid transporter, characterised in that the information contained in the nucleotide sequence allows, by integration in a plant genome, the formation of RNA, and with this RNA, a new amino acid transport activity can be introduced in the plant cells or an endogenous amino acid transporter activity can be expressed.
2. A DNA sequence according to claim 1, characterised in that, it contains the following nucleotide sequence (Seq-ID No 1):

CTTAAACAT TTATTTATC TTCTTCTTGT TCTCTCTTTC TCTTTCTCTC ATCACT 56

ATG AAG AGT TTC AAC ACA GAA GGA CAC AAC CAC TCC ACG GCG GAA 101  
Met Lys Ser Phe Asn Thr Glu Gly His Asn His Ser Thr Ala Glu  
1 5 10 15

TCC GGC GAT GCC TAC ACC GTG TCG GAC CCG ACA AAG AAC GTC GAT 146  
Ser Gly Asp Ala Tyr Thr Val Ser Asp Pro Thr Lys Asn Val Asp  
20 25 30

GAA GAT GGT CGA GAG AAG CGT ACC GGG ACG TGG CTT ACG GCG AGT 191  
Glu Asp Gly Arg Glu Lys Arg Thr Gly Thr Trp Leu Thr Ala Ser  
35 40 45

GCG CAT ATT ATC ACG GCG GTG ATA GGC TCC GGA GTG TTG TCT TTA 236  
Ala His Ile Ile Thr Ala Val Ile Gly Ser Gly Val Leu Ser Leu  
50 55 60

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GCA TGG GCT ATA GCT CAG CTT GGT TGG ATC GCA GGG ACA TCG ATC	281
Ala Trp Ala Ile Ala Gln Leu Gly Trp Ile Ala Gly Thr Ser Ile	
65 70 75	
TTA CTC ATT TTC TCG TTC ATT ACT TAC TTC ACC TCC ACC ATG CTT	326
Leu Leu Ile Phe Ser Phe Ile Thr Tyr Phe Thr Ser Thr Met Leu	
80 85 90	
GCC GAT TGC TAC CGT GCG CCG GAT CCC GTC ACC GGA AAA CGG AAT	371
Ala Asp Cys Tyr Arg Ala Pro Asp Pro Val Thr Gly Lys Arg Asn	
95 100 105	
TAC ACT TAC ATG GAC GTT GTT CGA TCT TAC CTC GGT GGT AGG AAA	416
Tyr Thr Tyr Met Asp Val Val Arg Ser Tyr Leu Gly Gly Arg Lys	
110 115 120	
GTG CAG CTC TGT GGA GTG GCA CAA TAT GGG AAT CTG ATT GGG GTC	461
Val Gln Leu Cys Gly Val Ala Gln Tyr Gly Asn Leu Ile Gly Val	
125 130 135	
ACT GTT GGT TAC ACC ATC ACT GCT TCT ATT AGT TTG GTA GCG GTA	506
Thr Val Gly Tyr Thr Ile Thr Ala Ser Ile Ser Leu Val Ala Val	
140 145 150	
GGG AAA TCG AAC TGC TTC CAC GAT AAA GGG CAC ACT GCG GAT TGT	551
Gly Lys Ser Asn Cys Phe His Asp Lys Gly His Thr Ala Asp Cys	
155 160 165	
ACT ATA TCG AAT TAT CCG TAT ATG GCG GTT TTT GGT ATC ATT CAA	596
Thr Ile Ser Asn Tyr Pro Tyr Met Ala Val Phe Gly Ile Ile Gln	
170 175 180	
GTT ATT CTT AGC CAG ATC CCA AAT TTC CAC AAG CTC TCT TTT CTT	641
Val Ile Leu Ser Gln Ile Pro Asn Phe His Lys Leu Ser Phe Leu	
185 190 195	

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TCC ATT ATG GCC GCA GTC ATG TCC TTT ACT TAT GCA ACT ATT GGA 686  
 Ser Ile Met Ala Ala Val Met Ser Phe Thr Tyr Ala Thr Ile Gly  
 200 205 210

ATC GGT CTA GCC ATC GCA ACC GTC GCA GGT GGG AAA GTG GGT AAG 731  
 Ile Gly Leu Ala Ile Ala Thr Val Ala Gly Gly Lys Val Gly Lys  
 215 220 225

ACG AGT ATG ACG GGC ACA GCG GTT GGA GTA GAT GTA ACC GCA GCT 776  
 Thr Ser Met Thr Gly Thr Ala Val Gly Val Asp Val Thr Ala Ala  
 230 235 240

CAA AAG ATA TGG AGA TCG TTT CAA GCG GTT GGG GAC ATA GCG TTC 821  
 Gln Lys Ile Trp Arg Ser Phe Gln Ala Val Gly Asp Ile Ala Phe  
 245 250 255

GCC TAT GCT TAT GCC ACG GTT CTC ATC GAG ATT CAG GAT ACA CTA 866  
 Ala Tyr Ala Tyr Ala Thr Val Leu Ile Glu Ile Gln Asp Thr Leu  
 260 265 270

AGA TCT AGC CCA GCT GAG AAC AAA GCC ATG AAA AGA GCA AGT CTT 911  
 Arg Ser Ser Pro Ala Glu Asn Lys Ala Met Lys Arg Ala Ser Leu  
 275 280 285

GTG GGA GTA TCA ACC ACC ACT TTT TTC TAC ATC TTA TGT GGA TGC 956  
 Val Gly Val Ser Thr Thr Thr Phe Phe Tyr Ile Leu Cys Gly Cys  
 290 295 300

ATC GGC TAT GCT GCA TTT GGA AAC AAT GCC CCT GGA GAT TTC CTC 1001  
 Ile Gly Tyr Ala Ala Phe Gly Asn Asn Ala Pro Gly Asp Phe Leu  
 305 310 315

ACA GAT TTC GGG TTT TTC GAG CCC TTT TGG CTC ATT GAC TTT GCA 1046  
 Thr Asp Phe Gly Phe Phe Glu Pro Phe Trp Leu Ile Asp Phe Ala  
 320 325 330

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AAC GCT TGC ATC GCT GTC CAC CTT ATT GGT GCC TAT CAG GTG TTC 1091  
 Asn Ala Cys Ile Ala Val His Leu Ile Gly Ala Tyr Gln Val Phe  
 335 340 345

GCG CAG CCG ATA TTC CAG TTT GTT GAG AAA AAA TGC AAC AGA AAC 1136  
 Ala Gln Pro Ile Phe Gln Phe Val Glu Lys Lys Cys Asn Arg Asn  
 350 355 360

TAT CCA GAC AAC AAG TTC ATC ACT TCT GAA TAT TCA GTA AAC GTA 1181  
 Tyr Pro Asp Asn Lys Phe Ile Thr Ser Glu Tyr Ser Val Asn Val  
 365 370 375

CCT TTC CTT GGA AAA TTC AAC ATT AGC CTC TTC AGA TTG GTG TGG 1226  
 Pro Phe Leu Gly Lys Phe Asn Ile Ser Leu Phe Arg Leu Val Trp  
 380 385 390

AGG ACA GCT TAT GTG GTT ATA ACC ACT GTT GTA GCT ATG ATA TTC 1271  
 Arg Thr Ala Tyr Val Val Ile Thr Thr Val Val Ala Met Ile Phe  
 395 400 405

CCT TTC TTC AAC GCG ATC TTA GGT CTT ATC GGA GCA GCT TCC TTC 1316  
 Pro Phe Phe Asn Ala Ile Leu Gly Leu Ile Gly Ala Ala Ser Phe  
 410 415 420

TGG CCT TTA ACG GTT TAT TTC CCT GTG GAG ATG CAC ATT GCA CAA 1361  
 Trp Pro Leu Thr Val Tyr Phe Pro Val Glu Met His Ile Ala Gln  
 425 430 435

ACC AAG ATT AAG AAG TAC TCT GCT AGA TGG ATT GCG CTG AAA ACG 1406  
 Thr Lys Ile Lys Lys Tyr Ser Ala Arg Trp Ile Ala Leu Lys Thr  
 440 445 450

ATG TGC TAT GTT TGC TTG ATC GTC TCG CTC TTA GCT GCA GCC GGA 1451  
 Met Cys Tyr Val Cys Leu Ile Val Ser Leu Leu Ala Ala Ala Gly  
 455 460 465

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TCC ATC GCA GGA CTT ATA AGT AGT GTC AAA ACC TAC AAG CCC TTC 1496  
 Ser Ile Ala Gly Leu Ile Ser Ser Val Lys Thr Tyr Lys Pro Phe  
 470 475 480

CGG ACT ATG CAT GAG TGAGTTTGAG ATCCTCAAGA GAGTCAAAAA 1541  
 Arg Thr Met His Glu  
 485

TATATGTAGT AGTTTGGTCT TTCTGTTAAA CTATCTGGTG TCTAAATCCA 1591

ATGAGAATGC TTTATTGCTA AACTTCATG AATCTCTCTG TATCTACATC 1641

TTTCAATCTA ATACATATGA GCTCTTCCAA AAAAAAAAAA AAAA 1685

3. A DNA sequence according to claim 1, characterised in that it contains the following nucleotide sequence (Seq-ID No 2):

CTATTTTAT AATTCCTCTT CTTTTTGTTT 29

ATAGCTTTGT AATTATAGTC TTATTCTCT TTAAGGCTCA ATAAGAGGAG 79

ATG GGT GAA ACC GCT GCC GCC AAT AAC CAC CGT CAC CAC CAC CAT 124  
 Met Gly Glu Thr Ala Ala Ala Asn Asn His Arg His His His His  
 1 5 10 15

CAC GGC CAC CAG GTC TTT GAC GTG GCC AGC CAC GAT TTC GTC CCT 169  
 His Gly His Gln Val Phe Asp Val Ala Ser His Asp Phe Val Pro  
 20 25 30

CCA CAA CCG GCT TTT AAA TGC TTC GAT GAT GAT GGC CGC CTC AAA 214  
 Pro Gln Pro Ala Phe Lys Cys Phe Asp Asp Asp Gly Arg Leu Lys  
 35 40 45

AGA ACT GGG ACT GTT TGG ACC GCG AGC GCT CAT ATA ATA ACT GCG 259  
 Arg Thr Gly Thr Val Trp Thr Ala Ser Ala His Ile Ile Thr Ala  
                     50                    55                    60

GTT ATC GGA TCC GGC GTT TTG TCA TTG GCG TGG GCG ATT GCA CAG 304  
 Val Ile Gly Ser Gly Val Leu Ser Leu Ala Trp Ala Ile Ala Gln  
                     65                    70                    75

CTC GGA TGG ATC GCT GGC CCT GCT GTG ATG CTA TTG TTC TCT CTT 349  
 Leu Gly Trp Ile Ala Gly Pro Ala Val Met Leu Leu Phe Ser Leu  
                     80                    85                    90

GTT ACT CTT TAC TCC TCC ACA CTT CTT AGC GAC TGC TAC AGA ACC 394  
 Val Thr Leu Tyr Ser Ser Thr Leu Leu Ser Asp Cys Tyr Arg Thr  
                     95                    100                    105

GGC GAT GCA GTG TCT GGC AAG AGA AAC TAC ACT TAC ATG GAT GCC 439  
 Gly Asp Ala Val Ser Gly Lys Arg Asn Tyr Thr Tyr Met Asp Ala  
                     110                    115                    120

GTT CGA TCA ATT CTC GGT GGG TTC AAG TTC AAG ATT TGT GGG TTG 484  
 Val Arg Ser Ile Leu Gly Gly Phe Lys Phe Lys Ile Cys Gly Leu  
                     125                    130                    135

ATT CAA TAC TTG AAT CTC TTT GGT ATC GCA ATT GGA TAC ACG ATA 529  
 Ile Gln Tyr Leu Asn Leu Phe Gly Ile Ala Ile Gly Tyr Thr Ile  
                     140                    145                    150

GCA GCT TCC ATA AGC ATG ATG GCG ATC AAG AGA TCC AAC TGC TTC 574  
 Ala Ala Ser Ile Ser Met Met Ala Ile Lys Arg Ser Asn Cys Phe  
                     155                    160                    165

CAC AAG AGT GGA GGA AAA GAC CCA TGT CAC ATG TCC AGT AAT CCT 619  
 His Lys Ser Gly Gly Lys Asp Pro Cys His Met Ser Ser Asn Pro  
                     170                    175                    180

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TAC ATG ATC GTA TTT GGT GTG GCA GAG ATC TTG CTC TCT CAG GTT 664  
 Tyr Met Ile Val Phe Gly Val Ala Glu Ile Leu Leu Ser Gln Val  
 185 190 200

CCT GAT TTC GAT CAG ATT TGG TGG ATC TCC ATT GTT GCA GCT GTT 709  
 Pro Asp Phe Asp Gln Ile Trp Trp Ile Ser Ile Val Ala Ala Val  
 205 210 220

ATG TCC TTC ACT TAC TCT GCC ATT GGT CTA GCT CTT GGA ATC GTT 754  
 Met Ser Phe Thr Tyr Ser Ala Ile Gly Leu Ala Leu Gly Ile Val  
 225 230 235

CAA GTT GCA GCG AAT GGA GTT TTC AAA GGA AGT CTC ACT GGA ATA 799  
 Gln Val Ala Ala Asn Gly Val Phe Lys Gly Ser Leu Thr Gly Ile  
 240 245 250

AGC ATC GGA ACA GTG ACT CAA ACA CAG AAG ATA TGG AGA ACC TTC 844  
 Ser Ile Gly Thr Val Thr Gln Thr Gln Lys Ile Trp Arg Thr Phe  
 255 260 265

CAA GCA CTT GGA GAC ATT GCC TTT GCG TAC TCA TAC TCT GTT GTC 889  
 Gln Ala Leu Gly Asp Ile Ala Phe Ala Tyr Ser Tyr Ser Val Val  
 270 275 280

CTA ATC GAG ATT CAG GAT ACT GTA AGA TCC CCA CCG GCG GAA TCG 934  
 Leu Ile Glu Ile Gln Asp Thr Val Arg Ser Pro Pro Ala Glu Ser  
 285 290 295

AAA ACG ATG AAG AAA GCA ACA AAA ATC AGT ATT GCC GTC ACA ACT 979  
 Lys Thr Met Lys Lys Ala Thr Lys Ile Ser Ile Ala Val Thr Thr  
 300 305 310

ATC TTC TAC ATG CTA TGT GGC TCA ATG GGT TAT GCC GCT TTT GGA 1024  
 Ile Phe Tyr Met Leu Cys Gly Ser Met Gly Tyr Ala Ala Phe Gly  
 315 320 325

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GAT GCA GCA CCG GGA AAC CTC CTC ACC GGT TTT GGA TTC TAC AAC 1069  
 Asp Ala Ala Pro Gly Asn Leu Leu Thr Gly Phe Gly Phe Tyr Asn  
 330 335 340

CCG TTT TGG CTC CTT GAC ATA GCT AAC GCC GCC ATT GTT GTC CAC 1114  
 Pro Phe Trp Leu Leu Asp Ile Ala Asn Ala Ala Ile Val Val His  
 245 350 355

CTC GTT GGA GCT TAC CAA GTC TTT GCT CAG CCC ATC TTT GCC TTT 1159  
 Leu Val Gly Ala Tyr Gln Val Phe Ala Gln Pro Ile Phe Ala Phe  
 360 365 370

ATT GAA AAA TCA GTC GCA GAG AGA TAT CCA GAC AAT GAC TTC CTC 1204  
 Ile Glu Lys Ser Val Ala Glu Arg Tyr Pro Asp Asn Asp Phe Leu  
 375 380 385

AGC AAG GAA TTT GAA ATC AGA ATC CCC GGA TTT AAG TCT CCT TAC 1249  
 Ser Lys Glu Phe Glu Ile Arg Ile Pro Gly Phe Lys Ser Pro Tyr  
 390 395 400

AAA GTA AAC GTT TTC AGG ATG GTP TAC AGG AGT GGC TTT GTC GTT 1294  
 Lys Val Asn Val Phe Arg Met Val Tyr Arg Ser Gly Phe Val Val  
 405 410 415

ACA ACC ACC GTG ATA TCG ATG CTG ATG CCG TTT TTT AAC GAC GTG 1339  
 Thr Thr Thr Val Ile Ser Met Leu Met Pro Phe Phe Asn Asp Val  
 420 425 430

GTC GGG ATC TTA GGG GCG TTA GGG TTT TGG CCC TTG ACG GTT TAT 1384  
 Val Gly Ile Leu Gly Ala Leu Gly Phe Trp Pro Leu Thr Val Tyr  
 435 440 445

TTT CCG GTG GAG ATG TAT ATT AAG CAG AGG AAG GTT GAG AAA TGG 1429  
 Phe Pro Val Glu Met Tyr Ile Lys Gln Arg Lys Val Glu Lys Trp  
 450 455 460

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AGC ACG AGA TGG GTG TGT TTA CAG ATG CTT AGT GTT GCT TGT CTT 1474  
 Ser Thr Arg Trp Val Cys Leu Gln Met Leu Ser Val Ala Cys Leu  
 465 470 475

GTG ATC TCG GTG GTC GCC GGG GTT GGA TCA ATC GCC GGA GTG ATG 1519  
 Val Ile Ser Val Val Ala Gly Val Gly Ser Ile Ala Gly Val Met  
 480 485 490

CTT GAT CTT AAG GTC TAT AAG CCA TTC AAG TCT ACA TAT 1558  
 Leu Asp Leu Lys Val Tyr Lys Pro Phe Lys Ser Thr Tyr  
 495 500

TGATGATTAT GGACCATGAA CAACAGAGAG AGTTGGTGTG TAAAGTTTAC 1608

CATTTCAAAG AAAACTCCAA AAATGTGTAT ATTGTATGTT GTTCTCATT 1658

CGTATGGTCT CATCTTTGTA ATAAAATTTA AAACCTTATGT TATAAATTAT 1708

AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AA 1740

4. A plasmid, characterised in that it contains a DNA sequence according to any one of claims 1 to 3.
5. Plasmid pPPP1-20 (DSM 7129).
6. Plasmid pAAP2, prepared according to Example 2.
7. Plasmid pBin PPP1-20 (DSM 7130).
- 10 8. Use of the plasmid according to any one of claims 4 to 7 or derivatives or parts thereof, for the transformation of prokaryotic and eukaryotic cells.
- 15 9. Plants containing a DNA sequence according to any one of claims 1 to 3.

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10. Bacteria containing a DNA sequence according to any one of claims 1 to 3.
- 5 11. Use of the DNA sequence of the amino acid transporter according to any one of claims 1 to 3 for the preparation of plasmids with changed specificity of the transporter.
- 10 12. Use of the DNA sequence of the amino acid transporter according to any one of claims 1 to 3 for isolation of similar sequences from the genome of the plant.
- 15 13. Use of the DNA sequence of the amino acid transporter according to any one of claims 1 to 3 for the expression of translatable mRNA, that makes possible the synthesis of an amino acid transporter in prokaryotic and eukaryotic cells.
- 20 14. Use of the DNA sequence of the amino acid transporter according to any one of claims 1 to 3 for the expression of a non-translatable mRNA, that hinders the synthesis of an amino acid transporter in prokaryotic and eukaryotic cells.
- 25 15. Use of the DNA sequence of the amino acid transporter according to any one of claims 1 to 3 in combination with steering elements for an expression in prokaryotic and eukaryotic cells.
- 30 16. Yeast strains containing DNA sequences according to any one of claims 1 to 3.
- 35 17. Use of yeast strains containing DNA sequences according to claim 16 for identification of a plant amino acid transporter.

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18. Use of the DNA sequence of the amino acid transporter according to any one of claims 1 to 3 for preparation of plants with changed amino acid and nitrogen metabolism.

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19. Use of the DNA sequence of the amino acid transporter according to any one of claims 1 to 3 for preparation of crop plants with increased yield.

10 20. Use of the DNA sequence of the amino acid transporter according to any one of claims 1 to 3 for the transport of compounds in prokaryotic and eukaryotic cells.

Add  
A2

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